

TTGTAACAGA AAATTAAAT ATACTCCACT CAAGGGAATT CTGTACTTTG CCCTTTTGGT -99  
 AAAGTCTCAT TTACATTTCT AACCTTTCT TAAGAAAATC GAATTTTCCTT TGATCTCTCT -39  
 1 TCTGAATTGC AGAAATCAGA TAAAACTAC TTGGTGAA ATG ACT TCT TGT CAC ATT 18  
 7 A E E H I Q K V A I F G G T H G  
 GCT GAA GAA CAT ATA CAA AAG GTT GCT ATC TTT GGA GGA ACC CAT GGG 66  
 23 N E L T G V F L V K H W L E N G  
 AAT GAG CTA ACC GGA GTA TTT CTG GTT AAG CAT TGG CTA GAG AAT GGC 114  
 39 A E I Q R T G L E V K P F I T N  
 GCT GAG ATT CAG AGA ACA GGG CTG GAG GTA AAA CCA TTT ATT ACT AAC 162  
 55 P R A V K K C T R Y I D C D L N  
 CCC AGA GCA GTG AAG AAG TGT ACC AGA TAT ATT GAC TGT GAC CTG AAT 210  
 71 R I F D L E N L G K K M S E D L  
 CGC ATT TTT GAC CTT GAA AAT CTT GGC AAA AAA ATG TCA GAA GAT TTG 258  
 87 P Y E V R R A Q E I N H L F G P  
 CCA TAT GAA GTG AGA AGG GCT CAA GAA ATA AAT CAT TTA TTT GGT CCA 306  
 103 K D S E D S Y D I I F D L H N T  
 AAA GAC AGT GAA GAT TCC TAT GAC ATT ATT TTT GAC CTT CAC AAC ACC 354  
 119 T S N M G C T L I L E D S R N N  
 ACC TCT AAC ATG GGG TGC ACT CTT ATT CTT GAG GAT TCC AGG AAT AAC 402  
 135 F L I Q M F H Y I K T S L A P L  
 TTT TTA ATT CAG ATG TTT CAT TAC ATT AAG ACT TCT CTG GCT CCA CTA 450  
 151 P C Y V Y L I E H P S L K Y A T  
 CCC TGC TAC GTT TAT CTG ATT GAG CAT CCT TCC CTC AAA TAT GCG ACC 498  
 167 T R S I A K Y P V G I E V G P Q  
 ACT CGT TCC ATA GCC AAG TAT CCT GTG GGT ATA GAA GTT GGT CCT CAG 546  
 183 P Q G V L R A D I L D Q M R K M  
 CCT CAA GGG GTT CTG AGA GCT GAT ATC TTG GAT CAA ATG AGA AAA ATG 594  
 199 I K H A L D F I H H F N E G K E  
 ATT AAA CAT GCT CTT GAT TTT ATA CAT CAT TTC AAT GAA GGA AAA GAA 642  
 215 F P P C A I E V Y K I I E K V D  
 TTT CCT CCC TGC GCC ATT GAG GTC TAT AAA ATT ATA GAG AAA GTT GAT 690  
 231 Y P R D E N G E I A A I I H P N  
 TAC CCC CGG GAT GAA AAT GGA GAA ATT GCT GCT ATC ATC CAT CCT AAT 738  
 247 L Q D Q D W K P L H P G D P M F  
 CTG CAG GAT CAA GAC TGG AAA CCA CTG CAT CCT GGG GAT CCC ATG TTT 786  
 263 L T L D G K T I P L G G D C T V  
 TTA ACT CTT GAT GGG AAG ACG ATC CCA CTG GGC GGA GAC TGT ACC GTG 834  
 279 Y P V F V N E A A Y Y E K K E A  
 TAC CCC GTG TTT GTG AAT GAG GCC GCA TAT TAC GAA AAG AAA GAA GCT 882  
 295 F A K T T K L T L N A K S I R C  
 TTT GCA AAG ACA ACT AAA CTA ACG CTC AAT GCA AAA AGT ATT CGC TGC 930  
 311 C L H  
 TGT TTA CAT TAG AA ATCACTTCCA GCTTACATCT TACACGGTGT CTTACAAATT 984  
 CTGCTAGTCT GTAAGCTCCT TAAGAGTAGG GTTGTGCCTT ATTCAACTGC ATACATAGCT 1044  
 CCTAGCACAG TGCCTTATTC GGTAGGCATC TAAGCAAATT TCTTAAATTA ATTAATATAT 1104  
 CTTTAAAGAT ATCATATTTT ATGTATGTAG CTTATTCAAA GAAGTGTTTC CTATTTCTAT 1164  
 ATAGTTTATT ATACATGATA CTTGGGTAGC TCAACATTCT TAATAAACAG CCTTTGTATT 1234  
 CAGAATATAA AATTGAAATA GATATATATA AAGTTAAAAA AAAAAAAAAA AAA 1287

Fig. 1

	10v	20v	30v	40v	50v
HLASP	MTSCHIAEEHIQKVAIFGGTHGNETGVFLVKHWLENGAEIQRTGLEVKPF				
	MTSCH:AE:.I:KVAIFGGTHGNETGVFLVKHWLEN::EIQRTGLEVKPF				
BASPCDNA	MTSCHVAEDPIKKVAIFGGTHGNETGVFLVKHWLENSTEIQRTGLEVKPF				
	10^	20^	30^	40^	50^
	60v	70v	80v	90v	100v
HLASP	ITNPRAVKKCTRYIDCDLNRIFDLENLGKKKSEDLPYEVRRRAQEINHFLFGP				
	ITNPRAVKKCTRYIDCDLNR:FD ENLGKK.SEDLPYEVRRRAQEINHFLFGP				
BASPCDNA	ITNPRAVKKCTRYIDCDLNRVFDPENLGKKKSEDLPYEVRRRAQEINHFLFGP				
	60^	70^	80^	90^	100^
	110v	120v	130v	140v	150v
HLASP	KDSSEDSYDIIIFDLHN*TTSNMGCTLILEDSRNNFLIQMFHYIKTSLAPLPCY				
	KDSSEDSYDIIIFDLHN*TTSNMGCTLILEDSRN:FLIQMFHYIKTSLAPLPCY				
BASPCDNA	KDSSEDSYDIIIFDLHN*TTSNMGCTLILEDSRNDFLIQMFHYIKTSLAPLPCY				
	110^	120^	130^	140^	150^
	160v	170v	180v	190v	200v
HLASP	VYLIEHPSLKYATTRSIAKYPVGIEVGPQPGVLRADILDQMRKMIKHALD				
	VYLIEHPSLKYATTRSIAKYPVGIEVGPQPGVLRADILDQMRKMI:HALD				
BASPCDNA	VYLIEHPSLKYATTRSIAKYPVGIEVGPQPGVLRADILDQMRKMIQHALD				
	160^	170^	180^	190^	200^
	210v	220v	230v	240v	250v
HLASP	FIHHFNEGKEFPPCAIEVYKIIIEKVDYPRDENGIEIAAIIHPNLQDQDWKPL				
	FIH:FNEGKEFPPCAIEVYKI: KVDYPR:E:GEI:AIHP:LQDQDWKPL				
BASPCDNA	FIHNFNEGKEFPPCAIEVYKIMRKVDYPRNESGEISAIHPKLQDQDWKPL				
	210^	220^	230^	240^	250^
	260v	270v	280v	290v	300v
HLASP	HPGDPMFLTLDGKTIPLGGDCTVYPVVFVNEAAYYEKKEAFAKTTKLTLNAK				
	HP.DP:FLTLDGKTIPLGGD TVYPVVFVNEAAYYEKKEAFAKTTKLTLNA:				
BASPCDNA	HPEDPVFLTLDGKTIPLGGDOTVYPVVFVNEAAYYEKKEAFAKTTKLTLNAN				
	260^	270^	280^	290^	300^
	310v				
HLASP	SIRCCLH				
	SIR..LH				
BASPCDNA	SIRSSLH				
	310^				

Fig. 2

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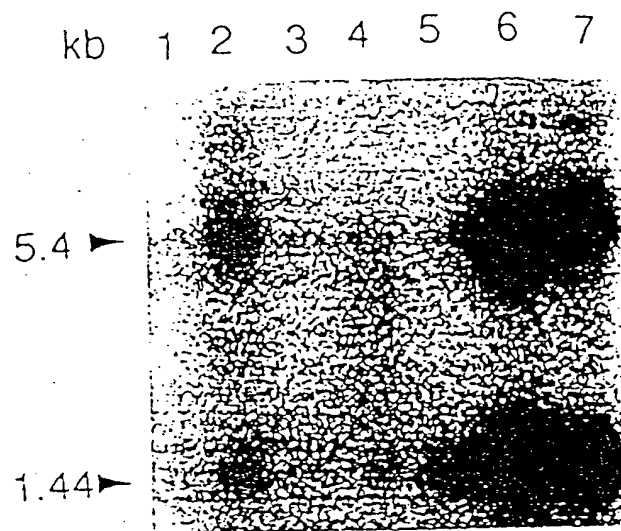


Fig. 3

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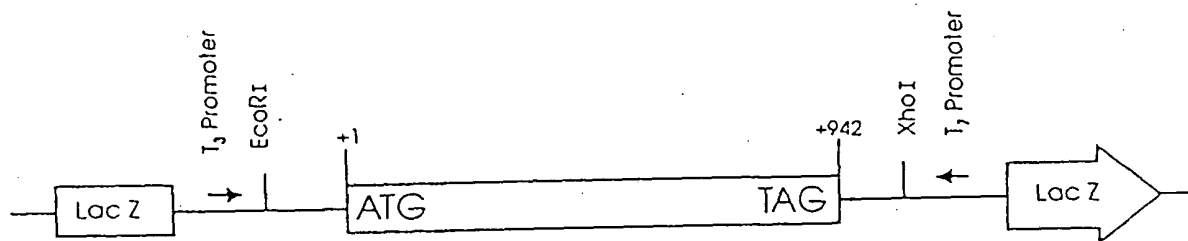


Fig. 4  
Kaul et al.

**A** A A T A T G C G C C T C A T T C A

WT

**B** A A T A T G C G C C G C A T T C A C

Mutant

Kaul et al.

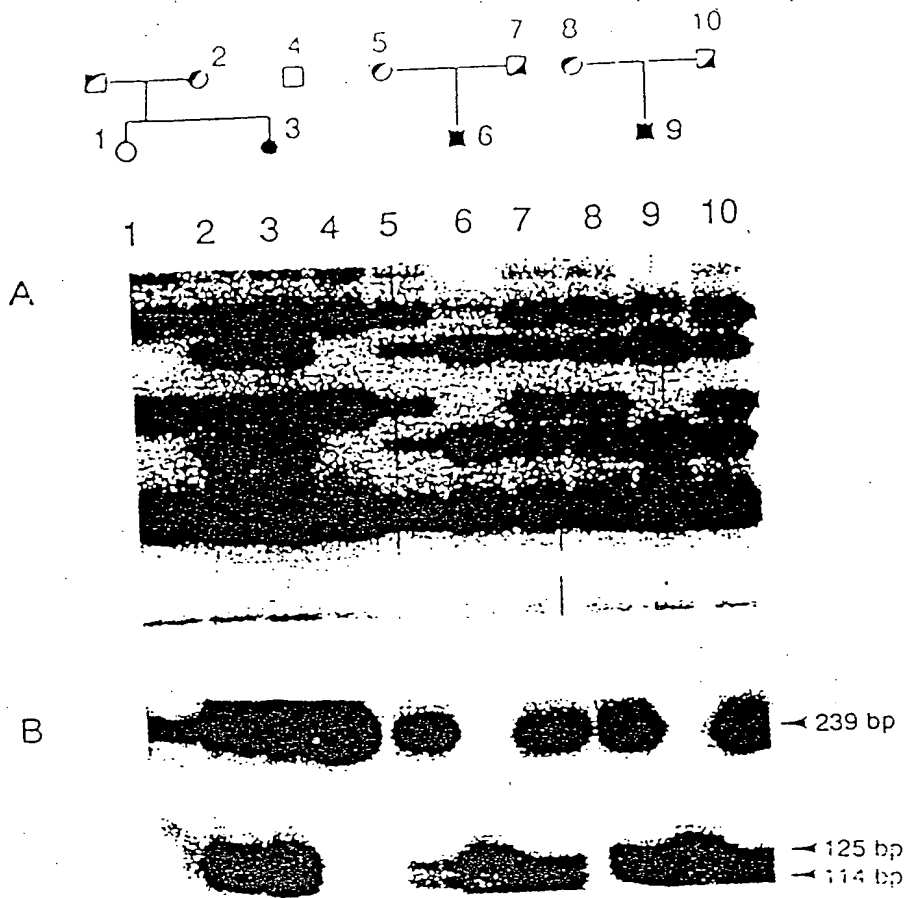


Fig. 6

Kaul et al.

8/26/93

EAM	M	E	M	N
ASA	B	C	N	L
MPE	O	5	L	A
1E3	2	7	1	4

ATGACTTCTTGTCACATTGCTGAAGAACATATACAAAAGGTTGCTATCTTTGGAGGAACC

Start site

-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 60  
TACTGAAGAACAGTGTAACGACTTCTTGTATATGTTTTCCAACGATAGAAACCTCCTTGG

m t s c h i a e e h i q k v a i f g g t

-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+

N	A	BBH	TSM	RM	H	HHD	TH
L	L	SCP	RPS	MA	I	HAD	FN
A	U	AAA	UOE	AE	N	AEE	IF
3	1	W72	911	11	P	121	11

CATGGGAATGAGCTAACCGGAGTATTTCTGGTTAAGCATTGGCTAGAGAATGGCGCTGAG

-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 120  
GTACCCTTACTCGATTGGCCTCATAAAGACCAATTTCGTAACCGATCTCTTACCGCGACTC

h g n e l t g v f l v k h w l e n g a e

-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+

M	B
N	P
L	M
1	1

ATTCAGAGAACAGGGCTGGAGGTAAAACCATTATTACTAACCCAGAGCAGTGAAGAAG

-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 180  
TAAGTCTCTTGTCCCACCTCCATTTTGGTAAATAATGATTGGGGTCTCGTCACTTCTTC

i q r t g l e v k p f i t n p r a v k k

-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+

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Restrict Sites

Fig. 7 (a)

67-15  
68-131  
132-141 17

CR	M	M	TH
SS	B	A	FN
PA	O	E	IF
61	2	3	11

TGTACCAGATATATTGACTGTGACCTGAATCGCATTTTTGACCTTGAAAATCTTGGCAAA

-----+-----+-----+-----+-----+-----+-----+-----+-----+  
 ACATGGTCTATATAACTGACACTGGACTTAGCGTAAAAACTGGAACCTTTTAGAACCGTTT

240

c t r y i d c d l n r i f d l e n l g k

-----+-----+-----+-----+-----+-----+-----+-----+-----+

NM	BN
DB	AS
EO	NP
12	22

AAAATGTCAGAAGATTTGCCATATGAAGTGAGAAGGGCTCAAGAAATAAATCATTATTT

-----+-----+-----+-----+-----+-----+-----+-----+-----+  
 TTTTACAGTCTTCTAAACGGTATACTTCACTCTTCCCGAGTTCTTTATTTAGTAAATAAA

300

k m s e d l p y e v r r a q e i n h l f

-----+-----+-----+-----+-----+-----+-----+-----+-----+

A	TH	M	S
V	FN	B	P
A	IF	O	O
2	11	2	1

GGTCCAAAAGACAGTGAAGATTCCTATGACATTATTTTTGACCTTCACAACACCACCTCT

-----+-----+-----+-----+-----+-----+-----+-----+-----+  
 CCAGGTTTTCTGTCACTTCTAAGGATACTGTAATAAAAACTGGAAGTGTTGTGGTGGAGA

360

g p k d s e d s y d i i f d l h n t t s

-----+-----+-----+-----+-----+-----+-----+-----+-----+

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Fig. 7(b)



MN A	HBN M	TH E AS	TM
NL P	GSS N	FN C PC	RS
LA L	IIP L	IF R YR	UE
13 1	AH2 1	11 2 11	91
/	//	/	/

AACATGGGGTGCACCTCTTATTCTTGAGGATTCCAGGAATAACTTTTTAATTCAGATGTTT  
 ---+---+---+---+---+---+---+---+---+ 420  
 TTGTACCCACGTGAGAATAAGAACTCCTAAGGTCCTTATTGAAAAATTAAGTCTACAAA

n m g c t l i l e d s r n n f l i q m f

---+---+---+---+---+---+---+---+---

TM	N	M F	E
RS	L	A O	C
UE	A	E K	O
91	4	2 1	B

CATTACATTAAGACTTCTCTGGCTCCACTACCCTGCTACGTTTATCTGATTGAGCATCCT  
 ---+---+---+---+---+---+---+---+--- 480  
 GTAATGTAATTCTGAAGAGACCGAGGTGATGGGACGATGCAAATAGACTAACTCGTAGGA

h y i k t s l a p l p c y v y l i e h p

---+---+---+---+---+---+---+---+---

S	M	A
F	N	V
A	L	A
N	1	2

TCCCTCAAATATGCGACCACTCGTTCCATAGCCAAGTATCCTGTGGGTATAGAAGTTGGT  
 ---+---+---+---+---+---+---+---+--- 540  
 AGGGAGTTTATACGCTGGTGAGCAAGGTATCGGTTTCATAGGACACCCATATCTTCAACCA

s l k y a t t r s i a k y p v g i e v g

---+---+---+---+---+---+---+---+---

Fig.7(c)

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D	M	M D	A	E	BMDD	TM
D	N	N D	L	C	IBPP	RS
E	L	L E	U	R	NONN	UE
1	1	1 1	1	V	1121	91

115 bp

CCTCAGCCTCAAGGGGTTCTGAGAGCTGATATCTTGGATCAAATGAGAAAAATGATTAAA  
 -----+-----+-----+-----+-----+-----+-----+  
 GGAGTCGGAGTTCCCCAAGACTCTCGACTATAGAACCTAGTTTACTCTTTTACTAATTT

600

p q p q g v l r a d i l d q m r k m i k

-----+-----+-----+-----+-----+-----+-----+

NN	HMHM
SL	INHN
PA	NLAL
H3	P111

CATGCTCTTGATTTTATACATCATTTCAATGAAGGAAAAGAATTTCTCCCTGCGCCATT  
 -----+-----+-----+-----+-----+-----+-----+  
 GTACGAGAACTAAAATATGTAGTAAAGTTACTTCCTTTTCTTAAAGGAGGGACGCGGTAA

660

h a l d f i h h f n e g k e f p p c a i

-----+-----+-----+-----+-----+-----+-----+

E	BSBNXSASSBBHNSB	FF	F	IF
C	SESCMMVCESSPCCB	OO	O	TN
P	ACAIAAARCAAAIRV	KK	K	AU
1	J1J111111JJ2111	11	1	1H

54 bp

GAGGTCTATAAAATTATAGAGAAAGTTGATTACCCCCGGGATGAAAATGGAGAAATTGCT  
 -----+-----+-----+-----+-----+-----+-----+  
 CTCCAGATATTTTAATATCTCTTTCAACTAATGGGGGCCCTACTTTTACCTCTTTAACGA

720

e v y k i i e k v d y p r d e n g e i a

-----+-----+-----+-----+-----+-----+-----+

c (93) > a  
 Y231 > X

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Fig. 7 (d)

S	PBMDD	F	ESASBBSBXBNMDDDB
F	SIBPP	O	CEPCSSFIHALBPPI
C	TNONN	K	RCYRAAANOMAONNN
1	11121	1	2111JJN12141211

GCTATCATCCATCCTAATCTGCAGGATCAAGACTGGAAACCACTGCATCCTGGGGATCCC  
 -----+-----+-----+-----+-----+-----+-----+-----+ 780  
 CGATAGTAGGTAGGATTAGACGTCCTAGTTCTGACCTTTGGTGACGTAGGACCCCTAGGG

a i i h p n l q d q d w k p l h p g d p

-----+-----+-----+-----+-----+-----+-----+-----+

19<sup>0</sup> 49 ✓

N	TM	B	MDBBBDBMA	BBAB	CR	CR
L	RS	B	BPBSPPIBL	SSCS	SS	SS
A	UE	V	ONSCUNNOW	ILIM	PA	PA
3	91	2	121911122	Y112	61	61

ATGTTTTTAACTCTTGATGGGAAGACGATCCCACTGGGCGGAGACTGTACCGTGTACCCC  
 -----+-----+-----+-----+-----+-----+-----+-----+ 840  
 TACAAAATTGAGAACTACCCTTCTGCTAGGGTGACCGCCTCTGACATGGCACATGGGG

m f l t l d g k t i p l g g d c t v y p

-----+-----+-----+-----+-----+-----+-----+-----+

SM	HIFA	H A
PN	ATNC	I L
OL	EAUI	N U
11	31H1	3 1

GTGTTTGTGAATGAGGCCGCATATTACGAAAAGAAAGAAGCTTTTGCAAAGACAACTAAA  
 -----+-----+-----+-----+-----+-----+-----+-----+ 900  
 CACAAACACTTACTCCGGCGTATAATGCTTTTCTTTCTTCGAAAACGTTTCTGTGATTT

v f v n e a a y y e k k e a f a k t t k

-----+-----+-----+-----+-----+-----+-----+-----+

0354>C  
 E285>A

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Fig. 7(e)

S	B	HIF	E	A
P	B	NTN	C	L
O	V	FAU	1	U
1	1	31H	5	1

Ala 305 > L  
C9147A

CTAACGCTCAATGCAAAAAGTATTCGCTGCTGTTTACATTAGAAATCACTTCCAGCTTAC  
-----+-----+-----+-----+-----+-----+-----+-----+-----+  
GATTGCGAGTTACGTTTTTCATAAGCGACGACAAATGTAATCTTTAGTGAAGGTCTGAATG

960

l t l n a k s i r c c l h . k s l p a y

-----+-----+-----+-----+-----+-----+-----+-----+-----+

RM	A	ATM
MA	L	FRS
AE	U	LUE
11	1	291

ATCTTACACGGTGTCTTACAAATTCTGCTAGTCTGTAAGCTCCTTAAGAGTAGGGTTGTG  
-----+-----+-----+-----+-----+-----+-----+-----+-----+  
TAGAATGTGCCACAGAATGTTTAAGACGATCAGACATTCGAGGAATTCTCATCCCAACAC

1020

i l h g v l q i l l v c k l l k s r v v

-----+-----+-----+-----+-----+-----+-----+-----+-----+

B	A	RM	H	D	S
S	L	MA	N	D	F
P	U	AE	F	E	A
W	1	11	3	1	N

CCTTATTCAACTGCATACATAGCTCCTAGCACAGTGCCTTATTCGGTAGGCATCTAAGCA  
-----+-----+-----+-----+-----+-----+-----+-----+-----+  
GGAATAAGTTGACGTATGTATCGAGGATCGTGTCACGGAATAAGCCATCCGTAGATTTCGT

1080

p y s t a y i a p s t v p y s v g i . a

-----+-----+-----+-----+-----+-----+-----+-----+-----+

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Fig. 7(f)

TM	ATM	PATM	TDM	E	A
RS	SRS	ASRS	RRS	C	L
UE	EUE	CEUE	UAE	R	U
91	191	1191	911	V	1

/        //        ///        /  
 AATTTCTTAAATTAATTAATATATCTTTAAAGATATCATATTTTATGTATGTAGCTTATT  
 -----+-----+-----+-----+-----+-----+-----+-----+ 1140  
 TTAAAGAATTTAATTAATTATATAGAAATTTCTATAGTATAAAATACATACATCGAATAA  
  
 n f l n . l i y l . r y h i l c m . l i

X	N	A
M	L	L
N	A	U
1	3	1

CAAAGAAGTGTTCCTATTTCTATATAGTTTATTATACATGATACTTGGGTAGCTCAACA  
 -----+-----+-----+-----+-----+-----+-----+ 1200  
 GTTTCCTTCACAAAGGATAAAGATATATCAAATAATATGTACTATGAACCCATCGAGTTGT  
  
 q r s v s y f y i v y y t . y l g s s t

✓  
 TM  
 RS  
 UE  
 91  
 /  
 TTCTTAATAAACAGCCTTTGTATTCAGAATATAAAATTGAAATAGATATATATAAAGTTA  
 -----+-----+-----+-----+-----+-----+-----+ 1260  
 AAGAATTATTTGTTCGAAACATAAGTCTTATATTTTAACTTTATCTATATATATTTCAAT  
  
 f l i n s l c i q n i k l k . i y i k l

AAAAAAAAAAAAAAAAAA  
 -----+-----+-----+-----+-----+-----+-----+ 1277  
 TTTTTTTTTTTTTTTTTT  
  
 k k k k k k

Fig. 7(g)

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